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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/775,803

DATE: 02/14/2001
 TIME: 16:33:28

ENTERED

Input Set : A:\Co5044us.txt
 Output Set: N:\CRF3\02142001\I775803.raw

2.

3 <110> APPLICANT: COR Therapeutics, Inc.
 4 Ramakrishnan, Vanitha
 5 Phillips, David
 7 <120> TITLE OF INVENTION: Transgenic Animals Having a Modified Glycoprotein V
 8 Gene and Methods for Their Use
 10 <130> FILE REFERENCE: 44481-5044-US
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/775,803
 C--> 13 <141> CURRENT FILING DATE: 2001-02-05
 15 <150> PRIOR APPLICATION NUMBER: PCT/US99/17594
 16 <151> PRIOR FILING DATE: 1999-08-04
 18 <150> PRIOR APPLICATION NUMBER: US 60/109,797
 19 <151> PRIOR FILING DATE: 1998-08-04
 21 <160> NUMBER OF SEQ ID NOS: 14
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 20
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 33 <220> FEATURE:
 34 <221> NAME/KEY: variation
 35 <222> LOCATION: (13)..(18)
 36 <223> OTHER INFORMATION: y at position 13 = c or t; r at position 18 = a or
 37 g.
 39 <400> SEQUENCE: 1
 40 ggcatgaccg tcytgcarcg 20
 43 <210> SEQ ID NO: 2
 44 <211> LENGTH: 7
 45 <212> TYPE: PRT
 46 <213> ORGANISM: Homo sapiens
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: Amino acid sequence corresponding to primer of
 50 seq. id no. 5.
 52 <400> SEQUENCE: 2
 53 Gly Met Thr Val Leu Gln Arg
 54 1 5
 57 <210> SEQ ID NO: 3
 58 <211> LENGTH: 23
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Artificial Sequence
 62 <220> FEATURE:
 63 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 65 <220> FEATURE:
 66 <221> NAME/KEY: variation
 67 <222> LOCATION: (3)..(21)
 68 <223> OTHER INFORMATION: y at position 3 = c or t; r at positions 6 and 21

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69      = a or g.
71 <400> SEQUENCE: 3
72      gayaaratgg tgytcytgga rca
75 <210> SEQ ID NO: 4
76 <211> LENGTH: 8
77 <212> TYPE: PRT
78 <213> ORGANISM: Homo sapiens
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Amino acid sequence corresponding to primer of
82      seq. id no. 7.
84 <400> SEQUENCE: 4
85      Asp Lys Met Val Leu Leu Glu Gln
86      1          5
89 <210> SEQ ID NO: 5
90 <211> LENGTH: 26
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
97 <220> FEATURE:
98 <221> NAME/KEY: variation
99 <222> LOCATION: (3)..(24)
100 <223> OTHER INFORMATION: y at positions 3, 12, 15, 18 and 19 = c or t; v at
101      position 6 = a or c or g; m at position 9 = a or
102      c; s at position 24 = c or g.
104 <400> SEQUENCE: 5
105      ccyyggvâcmâ tyâgygayyt gatsaa
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 9
110 <212> TYPE: PRT
111 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 6
114      Pro Gly Thr Phe Ser Asp Leu Ile Lys
115      1          5
118 <210> SEQ ID NO: 7
119 <211> LENGTH: 21
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
126 <220> FEATURE:
127 <221> NAME/KEY: variation
128 <222> LOCATION: (1)..(19)
129 <223> OTHER INFORMATION: r at positions 1, 7, 10, 13, 16 and 19 = a or g;
130      b at position 4 = c or g or t; k at position 6 =
131      g or t.
133 <400> SEQUENCE: 7
134      rttbckraar gcrâgcrâgcrâ g
137 <210> SEQ ID NO: 8

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23

26

21

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138 <211> LENGTH: 7
139 <212> TYPE: PRT
140 <213> ORGANISM: Homo sapiens
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Amino acid sequence corresponding to the
144     complementary strand of the primer in seq. id no.
145     11.
147 <400> SEQUENCE: 8
148     Pro Ala Ala Ala Phe Arg Asn
149     1          5
152 <210> SEQ ID NO: 9
153 <211> LENGTH: 29
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
160 <220> FEATURE:
161 <221> NAME/KEY: variation
162 <222> LOCATION: (8)..(27)
163 <223> OTHER INFORMATION: r at positions 8, 12, 15, 18, 23 and 27 = a or g;
164     k at position 9 = g or t.
166 <400> SEQUENCE: 9
167     ggccccarkc crcartcrca garccarga 29
170 <210> SEQ ID NO: 10
171 <211> LENGTH: 9
172 <212> TYPE: PRT
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 10
176     Ser Trp Arg Cys Asp Cys Gly Leu Gly
177     1          5
180 <210> SEQ ID NO: 11
181 <211> LENGTH: 3586
182 <212> TYPE: DNA
183 <213> ORGANISM: Mus musculus
185 <220> FEATURE:
186 <221> NAME/KEY: CDS
187 <222> LOCATION: (1411)..(3108)
188 <223> OTHER INFORMATION: Platelet glycoprotein V gene
190 <400> SEQUENCE: 11
191     gaattcattg gccttattta agaaataaaa tgttgagcaa aagagatggc tcatcaggta 60
193     aagatacctc ccaagacatg gtgtgagtcc ttgggaacct acgtggagga aggtgagaac 120
195     caattgccta aagttttctg acaccacaaa gtgaggcact gccacatgca cccacatact 180
197     cctgcacagg aatgagtttag tgcaatgtag catggaaaaa aacaaaaagt gtggcccatg 240
199     taatgacagc ctgctatttc tgggaaaact taggcctct actctctagc ttttcaaaaa 300
201     ggacttttaa ctatggactc tgaaagtttg aaagctcttg tcattaaaac ctagaatatg 360
203     ccctatggag atagtctttt tcttgacttt ttatctggta aggtctttat cttgaggatg 420
205     caagaatact tccctcttcc tctctgaagt gccaagtcac aagcagagct gcaagccttt 480
207     cagtcagtcc aggggtgcaga actgcttcag gtaaggccaa atattcttaa attagtgtat 540
209     gcagttagag gctcagtcctg tataggggca gaaggagacc tggtagaaga aacagtacaa 600

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211 atttttactt gggaaacaga gtaaactagt attactgtgt gcttcctggg taactcaatg 660
213 cccagagtag ttttattaag cagcttggtg tataagcaaa cagtagctca ttattttaa 720
215 gtgtgagtc gaaaaacatc ttcaaagtct acttatgtga cacttaaatt aacctcatgt 780
217 aactggagc gaccagccta ctgcactcgt gttactgtaa cagtgcagg ttcagaaaag 840
219 catggcataa agcaatgggc attatcacct gcaccactgg gctccggggc gggagttaca 900
221 aaacggtgta atgagttgtg ggggtgttggg actttgaaaa tatgtaagaa attgaatcta 960
223 gtggaagtgg gccttgctgc ggttctcttg ctgactgttg gggataaagc tccctgctta 1020
225 acttgttaaa gtcagtgcac cagccagtc caggaggcgt tgctttctat tctctgaaaa 1080
227 agaccgtagc aattttaatt cgttctgtaa cgattttaag gtattctgta gcttgaaaat 1140
229 gcccaaagt caatgctcta aacagaaccg gggagatggc tgactggata aaaatgggaa 1200
231 cctgtaagac tgatctactc tccaataccc acatatgctg aatagaaaag taattttttt 1260
233 ttaatcagcc tttgtaagat agaggaagac ttggttgat ctgagcgttc caaggccgtg 1320
235 agagtgcctg cccaaaaact gtgcttgac cagtgcgtgc agggctccag gatatgctct 1380
237 gagccttggt tttgctcttg catttcagac atg cta aga agc gcc ctg ctg tcc 1434
238                               Met Leu Arg Ser Ala Leu Leu Ser
239                               1               5
241 gcg gtg ctc gca ctc ttg cgt gcc caa cct ttt ccc tgc ccc aaa acc 1482
242 Ala Val Leu Ala Leu Leu Arg Ala Gln Pro Phe Pro Cys Pro Lys Thr
243      10               15               20
245 tgc aag tgt gtg gtc cgc gat gcc gcg cag tgc tcg ggc ggc agc gtg 1530
246 Cys Lys Cys Val Val Arg Asp Ala Ala Gln Cys Ser Gly Gly Ser Val
247      25               30               35               40
249 gct cac atc gct gag cta ggt ctg cct acg aac ctc aca cac atc ctg 1578
250 Ala His Ile Ala Glu Leu Gly Leu Pro Thr Asn Leu Thr His Ile Leu
251      45               50               55
253 ctc ttc cga atg gac cag ggc ata ttg cgg aac cac agc ttc agc ggc 1626
254 Leu Phe Arg Met Asp Gln Gly Ile Leu Arg Asn His Ser Phe Ser Gly
255      60               65               70
257 atg aca gtc ctt cag cgc ctg atg ctc tca gat agc cac att tcc gcc 1674
258 Met Thr Val Leu Gln Arg Leu Met Leu Ser Asp Ser His Ile Ser Ala
259      75               80               85
261 atc gac ccc ggc acc ttc aat gac ctg gta aaa ctg aaa acc ctc agg 1722
262 Ile Asp Pro Gly Thr Phe Asn Asp Leu Val Lys Leu Lys Thr Leu Arg
263      90               95               100
265 ttg acg cgc aac aaa atc tct cgt ctt cca cgt gcg atc ctg gat aag 1770
266 Leu Thr Arg Asn Lys Ile Ser Arg Leu Pro Arg Ala Ile Leu Asp Lys
267     105               110               115               120
269 atg gta ctc ttg gaa cag ctg ttc ttg gac cac aat gca cta agg gac 1818
270 Met Val Leu Leu Glu Gln Leu Phe Leu Asp His Asn Ala Leu Arg Asp
271      125               130               135
273 ctt gat caa aac ctg ttt cag caa ctg cgt aac ctt cag gag ctc ggt 1866
274 Leu Asp Gln Asn Leu Phe Gln Gln Leu Arg Asn Leu Gln Glu Leu Gly
275      140               145               150
277 ttg aac cag aat cag ctc tct ttt ctt cct gct aac ctt ttc tcg agc 1914
278 Leu Asn Gln Asn Gln Leu Ser Phe Leu Pro Ala Asn Leu Phe Ser Ser
279      155               160               165
281 ctg aga gaa ctg aag ttg ttg gat tta tcg cga aac aac ctg acc cac 1962
282 Leu Arg Glu Leu Lys Leu Leu Asp Leu Ser Arg Asn Asn Leu Thr His
283     170               175               180

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285	ctg ccc aag gga ctg ctt ggg gct caa gtt aag ctt gag aaa ctg ctg	2010
286	Leu Pro Lys Gly Leu Leu Gly Ala Gln Val Lys Leu Glu Lys Leu Leu	
287	185 190 195 200	
289	ctc tat tca aac cag ctc acg tct gtg gat tcg ggg ctg ctg agc aac	2058
290	Leu Tyr Ser Asn Gln Leu Thr Ser Val Asp Ser Gly Leu Leu Ser Asn	
291	205 210 215	
293	ctg ggc gcc ctg act gag ctg cgg ctg gag cgg aat cac ctc cgc tcc	2106
294	Leu Gly Ala Leu Thr Glu Leu Arg Leu Glu Arg Asn His Leu Arg Ser	
295	220 225 230	
297	gta gcc ccg ggt gcc ttc gac cgc ctc gga aac ctg agc tcc ttg act	2154
298	Val Ala Pro Gly Ala Phe Asp Arg Leu Gly Asn Leu Ser Ser Leu Thr	
299	235 240 245	
301	cta tcc gga aac ctc ctg gag tct ctg ccg ccc gcg ctc ttc ctt cac	2202
302	Leu Ser Gly Asn Leu Leu Glu Ser Leu Pro Pro Ala Leu Phe Leu His	
303	250 255 260	
305	gtg agc agc gtg tct cgg ctg act ctg ttc gag aac ccc ctg gag gag	2250
306	Val Ser Ser Val Ser Arg Leu Thr Leu Phe Glu Asn Pro Leu Glu Glu	
307	265 270 275 280	
309	ctc ccg gac gtg ttg ttc ggg gag atg gcc ggc ctg cgg gag ctg tgg	2298
310	Leu Pro Asp Val Leu Phe Gly Glu Met Ala Gly Leu Arg Glu Leu Trp	
311	285 290 295	
313	ctg aac ggc acc cac ctg agc acg ctg ccc gcc gct gcc ttc cgc aac	2346
314	Leu Asn Gly Thr His Leu Ser Thr Leu Pro Ala Ala Ala Phe Arg Asn	
315	300 305 310	
317	ctg agc ggc ttg cag acg ctg ggg ctg acg cgg aac ccg cgc ctg agc	2394
318	Leu Ser Gly Leu Gln Thr Leu Gly Leu Thr Arg Asn Pro Arg Leu Ser	
319	315 320 325	
321	gcg ctc ccg cgc ggc gtg ttc cag ggc cta cgg gag ctg cgc gtg ctc	2442
322	Ala Leu Pro Arg Gly Val Phe Gln Gly Leu Arg Glu Leu Arg Val Leu	
323	330 335 340	
325	gcg ctg cac acc aac gcc ctg gcg gag ctg cgg gac gac gcg ctg cgc	2490
326	Ala Leu His Thr Asn Ala Leu Ala Glu Leu Arg Asp Asp Ala Leu Arg	
327	345 350 355 360	
329	ggc ctc ggg cac ctg cgc cag gtg tcg ctg cgc cac aac cgg ctg cgg	2538
330	Gly Leu Gly His Leu Arg Gln Val Ser Leu Arg His Asn Arg Leu Arg	
331	365 370 375	
333	gcc ctg ccc cgc acg ctc ttc cgc aac ctc agc agc ctc gag agc gtg	2586
334	Ala Leu Pro Arg Thr Leu Phe Arg Asn Leu Ser Ser Leu Glu Ser Val	
335	380 385 390	
337	cag cta gag cac aac cag ctg gag acg ctg cca gga gac gtg ttc gcg	2634
338	Gln Leu Glu His Asn Gln Leu Glu Thr Leu Pro Gly Asp Val Phe Ala	
339	395 400 405	
341	gct ctg ccc cag ctg acc cag gtc ctg ctg ggt cac aac ccc tgg ctc	2682
342	Ala Leu Pro Gln Leu Thr Gln Val Leu Leu Gly His Asn Pro Trp Leu	
343	410 415 420	
345	tgc gac tgt ggc ctg tgg ccc ttc ctc cag tgg ctg cgg cat cac ccg	2730
346	Cys Asp Cys Gly Leu Trp Pro Phe Leu Gln Trp Leu Arg His His Pro	
347	425 430 435 440	
349	gac atc ctg ggc cga gac gag ccc ccg cag tgc cgt ggc ccg gag cca	2778

VERIFICATION SUMMARY
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Input Set : A:\Co5044us.txt
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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date